SEQUENCE LISTING

<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
      Molecules and Uses Therefor

<130> MPI2000-521P1R(M)

<140> US/10/024,036
<141> 2001-12-17

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<151> 2000-12-22

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cctccccagc gcgcccccgg ccgctcctcc gcgccgcgct cgtcggcc atg gcc cgg 177
                                                      Met Ala Arg
                                                        1

gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc   225

1

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             5               10               15

aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc    273
Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly Ala Phe Ser
 20               25               30               35

gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc ttt gct gtg    321
Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu Phe Ala Val
                 40               45               50

aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc agc ata gag    369
Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser Ser Ile Glu
                 55               60               65

aat gag ata gcc gtc ctg aga aag att aag cat gaa aat att gtt gcc    417
Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn Ile Val Ala
                 70               75               80

ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg gtc atg cag    465
Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu Val Met Gln
     85               90               95

ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag aag ggg ttt    513
Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
100               105               110               115

tat aca gag aag gat gcc agc act ctg atc cgc caa gtc ttg gac gcc    561
Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val Leu Asp Ala
                 120               125               130

gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac ctc aag ccc    609
Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp Leu Lys Pro
                 135               140               145

gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa ata atg atc    657
Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile
                 150               155               160

agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat gtg atg tcc    705
Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser
                 165               170               175

act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc ctc gcc cag    753
Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
180               185               190               195

aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga gtg att gcc    801
Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
                 200               205               210

tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa aat gac tcc    849
Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser
                 215               220               225

aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt gac tct ccc    897
Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro
                 230               235               240

tac tgg gat gac atc tcc gac tct gca aaa gac ttc att cgg aac ctg    945
Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu
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2

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atg gag aag gac ccg aat aaa aga tac acg tgt gag cag gca gct cgg    993
Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg
260             265             270             275

cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac atc cac gag   1041
His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu
                280             285             290

tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga   1089
Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg
                295             300             305

caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac   1137
Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His
                310             315             320

ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg agc agc ctc   1185
Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu
    325             330             335

agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa cca gaa tcc   1233
Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser
340             345             350             355

ctc agc tga cactgaagac gagcctgggg tggagaggag ggagccggca          1282
Leu Ser  *
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caacactttg ggaggctgag gcaggaggac tgtttgagtt caggagtttt aagaccagcc 1462
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Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
        35              40              45
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
    50              55              60
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
65              70              75              80
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
            85              90              95
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
            100             105             110
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
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                  115                     120                     125
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
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Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
145                     150                     155                     160
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
                 165                     170                     175
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
         195                     200                     205
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
         210                     215                     220
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
225                     230                     235                     240
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
                 245                     250                     255
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
         260                     265                     270
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
         275                     280                     285
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
         290                     295                     300
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
305                     310                     315                     320
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
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Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys
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gaagagaagg caactggcaa gctctttgct gtgaagtgta tccctaagaa ggcgctgaag  180
ggcaaggaaa gcagcataga gaatgagata gccgtcctga aaagattaa gcatgaaaat  240
attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggt catgcagctg  300
gtgtccggtg gagagctgtt tgaccggata gtggagaagg ggtttttatac agagaaggat  360
gccagcactc tgatccgcca agtcttggac gccgtgtact atctccacag aatgggcatc  420
gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa  480
ataatgatca gtgactttgg attgtcaaaa atggagggca aggagatgt gatgtccact  540
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gccgttgact gctggtccat cggagtgatt gcctacatct tgctctgcgg ctaccctcct  660
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gactctccct actgggatga catctccgac tctgcaaaag acttcattcg gaacctgatg  780
gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct  840
ggtgacacag ccctcaacaa aaacatccac gagtccgtca gcgcccagat ccggaaaaac  900
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aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgtttcgag cagcctcagt 1020
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<213> Homo sapiens

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tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttggag ggaaaaagta 180
cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
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ttagctgaca tctcagaagc cttgggctct cccagatgga agaatgaccg tgtgaggaaa 1140
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gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
              Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
              1               5                        10

gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc      1299
Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
     15                  20                  25

cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc      1347
Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
 30                  35                  40                  45

aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag      1395
Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
                 50                  55                  60

agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg      1443
Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
                 65                  70                  75

aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag      1491
Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
             80                  85                  90

aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc      1539
Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
         95                  100                 105

5

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agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt    1587
Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
110             115             120             125

ggg gtg gag att gaa aag acc tcg ggt gaa att atc aga tgc gag aag    1635
Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys
                130             135             140

tgc aag aga gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt    1683
Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu
            145             150             155

tct ctg ggg acc agt gag ctg gat atg ggg aag ggc cca atg tat gat    1731
Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp
            160             165             170

gtg gag aag ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca    1779
Val Glu Lys Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala
            175             180             185

aat cct gca agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc    1827
Asn Pro Ala Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser
190             195             200             205

agc ccc agg aat ccc act caa gag ctg agg aga ccc agc aag agc atg    1875
Ser Pro Arg Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met
            210             215             220

gac aag aaa gag gac aga ggc cca gag gat caa gaa agc cat gct cag    1923
Asp Lys Lys Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln
            225             230             235

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca    1971
Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr
            240             245             250

gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg    2019
Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg
            255             260             265

agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag    2067
Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu
270             275             280             285

aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa    2115
Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys
            290             295             300

aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa    2163
Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln
            305             310             315

cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag    2211
Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys
            320             325             330

cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc    2259
Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala
            335             340             345

gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg    2307
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6

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Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly
350             355             360             365

aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc   2355
Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala
                370             375             380

tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac   2403
Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp
                385             390             395

atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac   2451
Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn
                400             405             410

atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg   2499
Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu
                415             420             425

atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa   2547
Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu
430             435             440             445

agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta   2595
Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu
                450             455             460

tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac   2643
Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp
                465             470             475

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act   2691
Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr
                480             485             490

acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct   2739
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
                495             500             505

ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt   2787
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
510             515             520             525

tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg   2835
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
                530             535             540

atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag   2883
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
                545             550             555

agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag   2931
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
                560             565             570

ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg   2979
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
                575             580             585

gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat   3027
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
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7

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cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca   3075
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
                610                 615                 620

gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg   3123
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
                625                 630                 635

agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccacctt        3169
Ser Gln His Lys Arg Val Val Glu Gln Val Ser  *
                640                 645

gggaatctgt ccagccccca gttctgctca aggacagaga aaaggataga agtttgagag 3229
aaaaacaatg aaagaggctt cttcacataa ttggtgaatc agagggagag acactgagta 3289
tattttaaag catattaaaa aaattaagtc aatgttaaat gtcacaacat atttttagat 3349
ttgtatattt aaagccttta atacattttt ggggggtaag cattgtcatc agtgaggaat 3409
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agtggtgctt accagggtct aaactccccc tgtgagatta ataaggtgca ttgtggtctt 3529
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<212> PRT
<213> Homo sapiens

<400> 5

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            20                  25                  30
Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser Lys Ala Leu
        35                  40                  45
Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys Ser Cys Ser
    50                  55                  60
Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly Lys Ile Pro
65                  70                  75                  80
Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly
                85                  90                  95
Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala
            100                 105                 110
Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu
        115                 120                 125
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg
    130                 135                 140
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly
145                 150                 155                 160
Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys
                165                 170                 175
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala
            180                 185                 190
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg
            195                 200                 205
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys
    210                 215                 220
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala
225                 230                 235                 240
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly
                245                 250                 255
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His
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8

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                    260                 265                 270
Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg
        275                 280                 285
Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys
    290                 295                 300
Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys
305                 310                 315                 320
Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg
                325                 330                 335
Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val
            340                 345                 350
Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala
            355                 360                 365
Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met
    370                 375                 380
Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp
385                 390                 395                 400
Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys
                405                 410                 415
Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu
            420                 425                 430
Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys
            435                 440                 445
Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala
    450                 455                 460
Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro
465                 470                 475                 480
Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys
                485                 490                 495
Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr
            500                 505                 510
Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys
    515                 520                 525
Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr
            530                 535                 540
Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln
545                 550                 555                 560
Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro
                565                 570                 575
Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg
            580                 585                 590
Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu
            595                 600                 605
Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg
    610                 615                 620
Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His
625                 630                 635                 640
Lys Arg Val Val Glu Gln Val Ser
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agcaggctgt ttagcaaggc tctgaaagga gaccaccgct gtggggagac cgagaccccc 180
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9

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ggagagaagc atcttggggt ggagattgaa aagacctcgg gtgaaattat cagatgcgag 420
aagtgcaaga gagagaggga gctccagcag agcctggagc gtgagaggct ttctctgggg 480
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agaagctgca ggaggtctcc cgaggcaaat cctgcaagtg gggaggaagg gtggaagggt 600
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<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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     (Prosite Accession No. PS00107)

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<223> Leu can be Ile or Val.

<221> VARIANT
<222> 3
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> 5
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> 6
<223> Phe can be Tyr, Trp, Met, Gly, Ser, Thr, Asn, or
     His.

<221> VARIANT
<222> 7
<223> Ser can be Gly or Ala.

<221> VARIANT

10

<222> (8)...(8)
<223> Xaa can be any amino acid except Pro or Trp.

<221> VARIANT
<222> (9)...(9)
<223> Leu can be Ile, Val, Cys, Ala, or Thr.

<221> VARIANT
<222> (10)...(10)
<223> Xaa can be any amino acid except Pro or Asp.

<221> VARIANT
<222> (11)...(11)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (12)...(12)
<223> Gly can be Ser, Thr, Ala, Cys, Leu, Ile, Val, Met,
      Phe, or Tyr.

<221> VARIANT
<222> (13)...(13)
<223> Xaa can be any amino acid and asfew as 5 and as
      many as 18 amino acids.

<221> VARIANT
<222> (14)...(14)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser,
      Thr, Ala, or Arg.

<221> VARIANT
<222> (15)...(15)
<223> Ala can be Ile, Val, or Pro.

<221> VARIANT
<222> (16)...(16)
<223> Leu can be Ile, Val, Met, Phe, Ala, Gly, Cys. Lys,
      or Arg.

<221> BINDING
<222> (17)...(17)

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Lys

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for serine/threonine kinases
      (Prosite Accession No. PS00108)

<221> VARIANT
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<223> Leu can be Ile, Val, Met, Phe, or Tyr

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3
<223> His can be Tyr.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid.

<221> ACT_SITE
<222> 5

<221> VARIANT
<222> (6)...(6)
<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (8)...(9)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<400> 8
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 1               5               10


<210> 9
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for tyrosine kinase (Prosite
      Accession No. PS00109;

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<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3
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<223> His can be Tyr.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid.

<221> ACT_SITE
<222> 5

<221> VARIANT
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<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
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<223> Arg can be Ser, Thr, Ala, or Cys.

<221> VARIANT
<222> (8)...(9)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<400> 9
Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu
 1               5                   10


<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for tyrosine kinase
      phosphorylation site (Prosite Accession No.
      PS00007)

<221> VARIANT
<222> 1
<223> Arg can be Lys.

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid and can be two or three
      amino acids

<221> VARIANT
<222> 3
<223> Asp can be Glu.
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<221> VARIANT
<222> 4
<223> Xaa can be any amino acid and can be two or three
      amino acids

<221> PHOSPHORYLATION
<222> 5

<400> 10
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